

# FIG. 1

ATG ACC TGG AGG CAC CAT GTC AGG CTT CTG TTT ACG GTC AGT TTG GCA Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala	48
1                   5                   10                   15	
TTA CAG ATC ATC AAT TTG GGA AAC AGC TAT CAA AGA GAG AAA CAT AAC Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn	96
20                   25                   30	
GCG GGT AGA GGG GAA GTC ACC AAG GTT GCC ACT CAG AAG CAC CGA CAG Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln	144
35                   40                   45	
TCA CCG CTT AAC TGG ACC TCC AGT CAT TTC GGA GAG GTG ACT GGG AGC Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser	192
50                   55                   60	
GCC GAG GGC TGG GGG CCG GAG GAG CCG CTC CCC TAC TCC CCG GCT TTC Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe	240
65                   70                   75                   80	
GGA GAG GGT GCG TCC GCG CGG CCG CGC TGC TGC AGG AAC GGC GGT ACC Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr	288
85                   90                   95	
TGC GTG CTG GGC AGC TTC TGC GTG TGC CCG GCC CAC TTC ACC GGC CGC Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg	336
100                  105                  110	
TAC TGC GAG CAT GAC CAG AGG CGC AGT GAA TGC GGC GCC CTG GAG CAC Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His	384
115                  120                  125	
GGA GCC TGG ACC CTC CGC GCC TGC CAC CTC TGC AGG TGC ATC TTC GGG Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly	432
130                  135                  140	
GCC CTG CAC TGC CTC CCC CTC CAG ACG CCT GAC CGC TGT GAC CCG AAA Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys	480
145                  150                  155                  160	
GAC TTC CTG GCC TCC CAC GCT CAC GGG CCG AGC GCC GGG GGC GCG CCC Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro	528
165                  170                  175	
AGC CTG CTA CTC TTG CTG CCC TGC GCA CTC CTG CAC CGC CTC CTG CGC Ser Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg	576
180                  185                  190	
CCG GAT GCG CCC GCG CAC CCT CGG TCC CTG GTC CCT TCC GTC CTC CAG Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln	624
195                  200                  205	
CGG GAG CGG CGC CCC TGC GGA AGG CCG GGA CTT GGG CAT CGC CTT TAA Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu *	672
210                  215                  220	

# FIG. 2

## AMINO ACID ALIGNMENT BETWEEN CRIPTO AND CRIPTIN

	10	20	30	40	
1	M T W R H H V R L L F T V S L A L Q I I N L G N S Y Q R E K H N G G R G E V T K				HGS Cryptin
1	M - - H A A I S K V F E L G L - - - V A G L G - - - H Q E F A R P S R G Y L A -				Human Cripto
	50	60	70	80	
41	V A T Q K H R Q S P L N W T S S H F G E V T G S A E G W G P E E P L P Y S R A F				HGS Cryptin
32	- - - - F R D D S I - W P Q E E - P A I R P R S S Q R V P P P M G I Q H S K E L				Human Cripto
	90	100	110	120	
81	G E G A S A R P R C C R C N G G T C V L G S F C V C P A H F T G R Y C E H D Q R R				HGS Cryptin
65	N R T - - - - C C L N G G T C M L G S F C A C P P S F Y G R N C E H D V R K				Human Cripto
	130	140	150	160	
121	S E C G A L E H G A W T L R A C H L C R C I F G A L H C L P L Q T P D R C D P -				HGS Cryptin
99	E N C G S V P H D T W L P K K G S L C K C W H G Q L R C F P Q A F L P G C D G L				Human Cripto
	170	180	190	200	
160	- - - K D F L A S H A H G - P S A G G A P S L L L L P C A L L H R L L R P D A				HGS Cryptin
139	V M D E H L V A S R T P E L P P S A R T T F L M V G I C L S I Q S Y Y				Human Cripto
	210	220			
196	P A H P R S L V P S V L Q R E R R P C G R P G L G H R L				HGS Cryptin
174					Human Cripto

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.